



1/28

SEQUENCE LISTING

<110> Abbott Laboratories  
Mukerji, Pradip  
Huang, Yung-Sheng  
Pereira, Suzette L.

<120> DESATURASE GENES, ENZYMES ENCODED  
THEREBY, AND USES THEREOF

<130> 6884.US.01

<140> 10/060,793

<141> 2002-01-30

<160> 60

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atccgcgcgcg ccattcccaa gcaactgctgg gtcaag

36

<210> 2

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Forward Primer R01119

<221> misc\_feature

<222> (21)...(21)

<223> y = t/u or c at position 21

<221> misc\_feature

<222> (33)...(33)

<223> y = t/u or c at position 33

<400> 2

gccctcttcg tctcggcca ygactgcggc cayggctcgt tctcg

45

<210> 3

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse Primer R01118

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<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (30)...(31)
<223> r = g or a at positions 30-31

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (38)...(38)
<223> r = g or a at position 38

<221> misc_feature
<222> (39)...(39)
<223> y = t/u or c at position 39

<221> misc_feature
<222> (43)...(43)
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<223> y = t/u or c at position 9

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (36)...(36)
<223> y = t/u or c at position 36

<221> misc_feature
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<223> y = t/u or c at position 39

<400> 4

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 <212> DNA  
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<220>  
 <223> Reverse Primer R01122

<221> misc\_feature  
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 <223> r = g or a at position 7

<221> misc\_feature  
 <222> (10)...(10)  
 <223> r = g or a at position 10

<221> misc\_feature  
 <222> (37)...(37)  
 <223> r = g or a at position 37

<400> 5  
 gttctgtrtgr tgggtccgrt gcgagatgcg ccagccrtgg taggg

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<210> 6  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<221> misc\_feature  
 <222> (13)...(13)  
 <223> s = g or c at position 13

<221> misc\_feature  
 <222> (19)...(19)  
 <223> k = g or t/u at position 19

<400> 6  
 ggctcgact tcsaccccka ctcgacctc ttcgtc

36

<210> 7  
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<220>  
 <223> Reverse Primer R01147

<221> misc\_feature  
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 <223> m = a or c at position 18

<221> misc\_feature

<222> (24)...(24)  
 <223> w = a or t/u at position 24

<400> 7  
 gacgaagagg tccgagtmgg ggtwgaagtg cgagcc

36

<210> 8  
 <211> 39  
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<220>  
 <223> Reverse Primer RO1148

<221> misc\_feature  
 <222> (9)...(9)  
 <223> k = g or t/u at position 9

<221> misc\_feature  
 <222> (30)...(30)  
 <223> w = a or t/u at position 30

<221> misc\_feature  
 <222> (32)...(32)  
 <223> s = g or c at position 32

<400> 8  
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39

<210> 9  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Reverse Primer RO1114

<221> misc\_feature  
 <222> (13)...(13)  
 <223> r = g or a at position 13

<221> misc\_feature  
 <222> (16)...(16)  
 <223> r = g or a at position 16

<221> misc\_feature  
 <222> (25)...(25)  
 <223> r = g or a at position 25

<221> misc\_feature  
 <222> (40)...(40)  
 <223> r = g or a at position 40

<221> misc\_feature  
 <222> (43)...(43)  
 <223> r = g or a at position 43

<400> 9  
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<210> 10  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
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<221> misc\_feature  
<222> (12)...(12)  
<223> y = t/u or c at position 12

<221> misc\_feature  
<222> (16)...(16)  
<223> r = g or a at position 16

<221> misc\_feature  
<222> (22)...(22)  
<223> r = g or a at position 22

<221> misc\_feature  
<222> (33)...(33)  
<223> k = g or t/u at position 33

<221> misc\_feature  
<222> (42)...(43)  
<223> r = g or at at positions 42-43

<400> 10  
ggtggcctcg aygagrtggt artgggggat ctkggggaag arrtg

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<210> 11  
<211> 45  
<212> DNA  
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<223> Reverse Primer R01118

<221> misc\_feature  
<222> (4)...(4)  
<223> r = g or a at position 4

<221> misc\_feature  
<222> (10)...(10)  
<223> r = g or a at position 10

<221> misc\_feature  
<222> (30)...(31)  
<223> r = g or a at positions 30-31

<221> misc\_feature  
<222> (34)...(34)  
<223> r = g or a at position 34

<221> misc\_feature  
 <222> (38)...(38)  
 <223> r = g or a at position 38

<221> misc\_feature  
 <222> (39)...(39)  
 <223> y = t/u or c at position 39

<221> misc\_feature  
 <222> (43)...(43)  
 <223> r = g or a at position 43

<400> 11  
 gagrtggtar tgggggatct gggggaagar rtgrtggrg acrtg 45

<210> 12  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer R01188

<400> 12  
 tacgcgtacc tcacgtactc gctcg 25

<210> 13  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer R01189

<400> 13  
 ttcttgacc acaacgacga agcgacg 27

<210> 14  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer R01190

<400> 14  
 ggagtggacg tacgtcaagg gcaac 25

<210> 15  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer R01191

<400> 15  
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 <210> 16  
 <211> 31  
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 <223> Primer R0898  
  
 <400> 16  
 cccagtcacg acgttgtaaa acgacggcca g 31  
  
 <210> 17  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Primer R0899  
  
 <400> 17  
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 <210> 18  
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 <223> Reverse Primer R01185  
  
 <400> 18  
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 <211> 20  
 <212> DNA  
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 <223> Reverse Primer R01186  
  
 <400> 19  
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 <210> 20  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Reverse Primer R01187  
  
 <400> 20  
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<210> 21  
 <211> 45  
 <212> DNA  
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<220>  
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<400> 21  
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<210> 22  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Reverse Primer RO1213

<400> 22  
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<210> 23  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer RO1221

<400> 23  
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<210> 24  
 <211> 45  
 <212> DNA  
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<220>  
 <223> Reverse Primer RO1222

<400> 24  
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<210> 25  
 <211> 1077  
 <212> DNA  
 <213> Saprolegnia diclina

<400> 25  
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 ttcaacgcgt cggcctcggc ggcgtgctc tacggggcgc gctcgacgcc gttcattgcc 180  
 gataacgttc tgctccacgc gctcgtttgc gccacctaca tctacgtgca gggcgatcac 240  
 ttctggggct tcttcacggc cggccacgac tgcggccact cggccttctc gcgctaccac 300  
 agcgtcaact ttatcatcgg ctgcatcatg cactctgcga ttttgacgcc gttcgagagc 360



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tggcgcgtga cgcaccgcca ccaccacaag aacacgggca acattgataa ggacgagatc 420
ttttaccgcg accggtcggg caaggacctc caggacgtgc gccaatgggt ctacacgctc 480
ggcgggtgcgt ggtttgtcta cttgaaggtc gggatatgcc cgcgcacgat gagccacttt 540
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&lt;210&gt; 26

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Saprolegnia diclina

&lt;400&gt; 26

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Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
 1          5          10          15
Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
 20          25          30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
 35          40          45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
 50          55          60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
 65          70          75          80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
 85          90          95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
 100          105          110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
 115          120          125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
 130          135          140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
 145          150          155          160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
 165          170          175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
 180          185          190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
 195          200          205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
 210          215          220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
 225          230          235          240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
 245          250          255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
 260          265          270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
 275          280          285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
 290          295          300

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Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile  
 305 310 315 320  
 Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala  
 325 330 335  
 Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala  
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 Ala Lys Ala Lys Ser Asp  
 355

<210> 27  
 <211> 1413  
 <212> DNA  
 <213> Saprolegnia diclina

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 atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc 180  
 cgcgagatgg tgctgctgca cgccggctgc gagggccacc acacgttcga ctcgtagcac 240  
 ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gtacacgggc 300  
 ccgtccgagt ttccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc 360  
 gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg 420  
 cgcatgatgg tcgtgtttgc ggtcgccggc ctgccttgt acggcatgca ctttctgact 480  
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 gtgctcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac 660  
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<210> 28  
 <211> 819  
 <212> DNA  
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 accatgctgg cattcgaggt gggatacatg gccatgtctg tcttcggcat cccgatcatg 180  
 aagcagatgg agaagccttt tgagctcaag accatcaagc tcttgacaaa ctgtttctc 240  
 ttcggacttt ccttgatcat gtgcgtggag accatccgcc aggtatcct cggaggctac 300  
 aaagtgtttg gaaacgacat ggagaagggc aacgagtctc atgctcaggg catgtctcgc 360  
 atcgtgtacg tgttctgcgt gtccaaggca tacgagttct tggataccgc catcatgatc 420  
 ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccattttt 480  
 gccatctggt gggctatcgc caagtacgct ccaggagggt atgcgtactt tcagtgtac 540  
 ctcaactctt tcgtgcacac cgtcatgtac gcatactact tcttctcctc ccaagggttc 600  
 gggttcgtga agccaatcaa gccgtacatc accacccttc agatgacca gttcatggca 660

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atgcttgtgc agtccttgta cgactacctc ttcccatgcg actaccacaca ggctcttgtg 720
cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag 780
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&lt;210&gt; 29

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Saprolegnia diclina

&lt;400&gt; 29

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Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
 1          5          10          15
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
      20          25          30
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
      35          40          45
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
      50          55          60
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
      65          70          75          80
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp
      85          90          95
Ser Ala Ser Tyr Trp Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
      100          105          110
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
      115          120          125
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
      130          135          140
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
      145          150          155          160
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys
      165          170          175
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met
      180          185          190
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met
      195          200          205
Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu
      210          215          220
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp
      225          230          235          240
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr
      245          250          255
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys
      260          265          270
Phe Gln His Leu Tyr Ala Pro Leu Ile Phe Gly Phe Met Thr Ile Asn
      275          280          285
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe
      290          295          300
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Asn Val Ala Arg
      305          310          315          320
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro
      325          330          335
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala
      340          345          350
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His
      355          360          365
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val

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<210> 30
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO967

<221> misc_feature
<222> (4)...(4)
<223> s = g or c at position 4

<221> misc_feature
<222> (12)...(12)
<223> s = g or c at position 12

<221> misc_feature
<222> (30)...(30)
<223> s = g or c at position 30

<221> misc_feature
<222> (31)...(31)
<223> k = g or t/u at position 31

<221> misc_feature
<222> (32)...(32)
<223> s = g or c at position 32
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51

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<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
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<223> Reverse Primer R0968

<221> misc\_feature

<222> (2)...(2)

<223> r = g or a at position 2

<221> misc\_feature

<222> (3)...(3)

<223> s = g or c at position 3

<221> misc\_feature

<222> (12)...(12)

<223> k = g or t/u at position 12

<221> misc\_feature

<222> (17)...(17)

<223> w = a or t/u at position 17

<221> misc\_feature

<222> (18)...(18)

<223> m = a or c at position 18

<221> misc\_feature

<222> (19)...(19)

<223> s = g or c at position 19

<221> misc\_feature

<222> (41)...(41)

<223> w = a or t/u at position 41

<221> misc\_feature

<222> (42)...(42)

<223> r = g or a at position 42

<400> 31

grscttcttg akgtggwmsg tggcctcctc ggcgtggtag wrccgcat

48

<210> 32

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer R0964

<221> misc\_feature

<222> (3)...(4)

<223> s = g or c at positions 3-4

<221> misc\_feature

<222> (25)...(25)

<223> r = g or a at position 25

<221> misc\_feature

<222> (36)...(36)

<223> s = g or c at position 36

<400> 32  
ccsstctact gggcctgccca gggtrtcgtc ctcacsggtg tctgg

45

<210> 33  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (16)...(16)  
<223> r = g or a at position 16

<221> misc\_feature  
<222> (17)...(17)  
<223> y = t/u or c at position 17

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<221> misc\_feature  
<222> (25)...(25)  
<223> r = g or a at position 25

<221> misc\_feature  
<222> (31)...(31)  
<223> k = g or t/u at position 31

<221> misc\_feature  
<222> (33)...(33)  
<223> y = t/u or c at position 33

<221> misc\_feature  
<222> (36)...(36)  
<223> s = g or c at position 36

<400> 33  
ccsstctact ggatcrysca gggtrtcgtc kgyacsggtg tctgg

45

<210> 34  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse Primer R0966

<221> misc\_feature  
<222> (19)...(19)  
<223> s = g or c at position 19

<221> misc\_feature  
 <222> (20)...(21)  
 <223> m = a or c at positions 20-21  
  
 <221> misc\_feature  
 <222> (30)...(30)  
 <223> r = g or a at position 30  
  
 <400> 34  
 ggcgtaggtg tgcggcatism mcgagaagar gtggtgggacg acgtg 45  
  
 <210> 35  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Forward Primer R0975  
  
 <400> 35  
 cacgtacctc cagcacacgg acacctacg 29  
  
 <210> 36  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Forward Primer R0976  
  
 <400> 36  
 gatcgacagc gcgatccacc acattgc 27  
  
 <210> 37  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Reverse Primer R0977  
  
 <400> 37  
 caaatggtaa aagctagtgg cagcgctgc 29  
  
 <210> 38  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Reverse Primer R0978  
  
 <400> 38  
 agtacgtgcc ctggacgaac cagtagatg 29  
  
 <210> 39

<211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Forward Primer R01051

<400> 39  
 tcaacagaat tcatgtgcaa aggtcaagct ccttccaagg ccgacgtg 48

<210> 40  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Reverse Primer R01057

<400> 40  
 aaaagaaagc ttttactttt cctcgagctt gcgcttgtaa aacacaac 48

<210> 41  
 <211> 1182  
 <212> DNA  
 <213> Saprolegnia diclina

<400> 41  
 atgtgcaaag gtcaagctcc ttccaaggcc gacgtgttcc acgctgcggg gtaccgcccg 60  
 gtcgccggca cgcccgagcc gctgccgctg gagccccga cgatcacgct caaggacctg 120  
 cgcgcgggca tcccggccca ctgctttgag cgacgcgctg ccactagctt ttaccatttg 180  
 gccaaagaacc ttgcgatctg cgccggcggtg ttgcgcgttg gcctcaagct cgcggtgccc 240  
 gacttgccgc tcgcggccaa gctggtcgcg tggcccatct actggttcgt ccagggcacg 300  
 tacttttacgg gcatctgggt cattgcgcac gaatgcggcg accaggcggt ctgcgcgtcc 360  
 gagatcctca acgacacggg cggtatcatt ctccactcgc tccctcttgg gccgtaccac 420  
 agctggaaga tcacgcaccg ccgccaccac tccaacacgg gcagctgcga gaacgacgag 480  
 gtgttttacgc cgacgcgcgc gtccgtcgtc gaggccaagc acgaccactc gtcctcga 540  
 gagagcccgc tctacaacct gtacggcatc gtcgatgatc ttctcgtggg ctggatgccg 600  
 ggctacctct tcttcaacgc gaccggcccg accaagtagc ctggcctcgc caagtcgcac 660  
 ttcaaccctg acgcagcctt tttcctccca aaggagcgcc tcagcatctg gtggagcgac 720  
 ctctgcttcc tcgcggcctt gtacggcttt ggctacggcg tctcgggtct cggcctcctc 780  
 gatgtcgccc gccactacat cgtgccgtac ctcatcttga acgcgtacct cgtgctcatc 840  
 acgtacctcc agcacacgga tacgtacgtg cccacttcc gcggcgacga gtggaactgg 900  
 ctgcgcggcg cgctctgcac cgtcgaccgc tcgttcggcg cgtggatcga cagcgcgatc 960  
 caccacattg ccgacacgca cgtgacgcac cacattttct ccaagacgcc cttctaccac 1020  
 gcgatcgagg cgaccgacgc catcacgccc ctctcgggca agtactacct catcgaccgc 1080  
 acgccgatcc cgctggcgct ctggcgctcg ttcacgcact gcaagtagct cgaggacgac 1140  
 ggcaacgttg tgttttataa gcgcaagctc gaggaaaagt aa 1182

<210> 42  
 <211> 393  
 <212> PRT  
 <213> Saprolegnia diclina

<400> 42  
 Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala  
 1 5 10 15  
 Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro



```
<210> 43
<211> 393
<212> PRT
<213> Saprolegnia diclina
```

```
<400> 43
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
 1             5             10             15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
```

			20					25					30			
Pro	Thr	Ile	Thr	Leu	Lys	Asp	Leu	Arg	Ala	Ala	Ile	Pro	Ala	His	Cys	
		35					40					45				
Phe	Glu	Arg	Ser	Ala	Ala	Thr	Ser	Phe	Tyr	His	Leu	Ala	Lys	Asn	Leu	
	50					55					60					
Ala	Ile	Cys	Ala	Gly	Val	Phe	Ala	Val	Gly	Leu	Lys	Leu	Ala	Ala	Ala	
65					70					75					80	
Asp	Leu	Pro	Leu	Ala	Ala	Lys	Leu	Val	Ala	Trp	Pro	Ile	Tyr	Trp	Phe	
				85						90				95		
Val	Gln	Gly	Thr	Tyr	Phe	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	
			100					105					110			
Gly	His	Gln	Ala	Phe	Ser	Ala	Ser	Glu	Ile	Leu	Asn	Asp	Thr	Val	Gly	
		115					120					125				
Ile	Ile	Leu	His	Ser	Leu	Leu	Phe	Val	Pro	Tyr	His	Ser	Trp	Lys	Ile	
	130					135					140					
Thr	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Cys	Glu	Asn	Asp	Glu	
145				150						155					160	
Val	Phe	Thr	Pro	Thr	Pro	Arg	Ser	Val	Val	Glu	Ala	Lys	His	Asp	His	
				165						170				175		
Ser	Leu	Leu	Glu	Glu	Ser	Pro	Leu	Tyr	Asn	Leu	Tyr	Gly	Ile	Val	Met	
			180					185					190			
Met	Leu	Leu	Val	Gly	Trp	Met	Pro	Gly	Tyr	Leu	Phe	Phe	Asn	Ala	Thr	
		195					200					205				
Gly	Pro	Thr	Lys	Tyr	Ala	Gly	Leu	Ala	Lys	Ser	His	Phe	Asn	Pro	Tyr	
	210					215					220					
Ala	Ala	Phe	Phe	Leu	Pro	Lys	Glu	Arg	Leu	Ser	Ile	Trp	Trp	Ser	Asp	
225				230						235					240	
Leu	Cys	Phe	Leu	Ala	Ala	Leu	Tyr	Gly	Phe	Gly	Tyr	Gly	Val	Ser	Val	
				245					250					255		
Phe	Gly	Leu	Leu	Asp	Val	Ala	Arg	His	Tyr	Ile	Val	Pro	Tyr	Leu	Ile	
			260					265					270			
Cys	Asn	Ala	Tyr	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	Asp	Thr	
	275						280					285				
Tyr	Val	Pro	His	Phe	Arg	Gly	Asp	Glu	Trp	Asn	Trp	Leu	Arg	Gly	Ala	
	290					295				300						
Leu	Cys	Thr	Val	Asp	Arg	Ser	Phe	Gly	Ala	Trp	Ile	Asp	Ser	Ala	Ile	
305				310						315					320	
His	His	Ile	Ala	Asp	Thr	His	Val	Thr	His	His	Ile	Phe	Ser	Lys	Thr	
				325					330					335		
Pro	Phe	Tyr	His	Ala	Ile	Glu	Ala	Thr	Asp	Ala	Ile	Thr	Pro	Leu	Leu	
			340					345					350			
Gly	Lys	Tyr	Tyr	Leu	Ile	Asp	Pro	Thr	Pro	Ile	Pro	Leu	Ala	Leu	Trp	
	355					360					365					
Arg	Ser	Phe	Thr	His	Cys	Lys	Tyr	Val	Glu	Asp	Asp	Gly	Asn	Val	Val	
	370					375										

<210> 44

<211> 359

&lt;212&gt; PRT

<213> Synechocystis sp.

 $\langle 220 \rangle$ 

## <221> VARIANT

 $\langle 222 \rangle \quad (315) \dots (315)$ 

<223> Xaa = Unknown or Other at position 315

&lt;221&gt; VARIANT

&lt;222&gt; (331)...(331)

&lt;223&gt; Xaa = Unknown or Other at position 331

&lt;400&gt; 44

```

Tyr Phe Phe Leu Asp Val Gly Leu Ile Ala Gly Phe Tyr Ala Leu Ala
 1           5           10           15
Ala Tyr Leu Asp Ser Trp Phe Phe Tyr Pro Ile Phe Trp Leu Ile Gln
          20           25           30
Gly Thr Leu Phe Trp Ser Leu Phe Val Val Gly His Asp Cys Gly His
          35           40           45
Gly Ser Phe Ser Lys Ser Lys Thr Leu Asn Asn Trp Ile Gly His Leu
          50           55           60
Ser His Thr Pro Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His
          65           70           75           80
Arg Thr His His Ala Asn Thr Gly Asn Ile Asp Thr Asp Glu Ser Trp
          85           90           95
Tyr Pro Val Ser Glu Gln Lys Tyr Asn Gln Met Ala Trp Tyr Glu Lys
          100          105          110
Leu Leu Arg Phe Tyr Leu Pro Leu Ile Ala Tyr Pro Ile Tyr Leu Phe
          115          120          125
Arg Arg Ser Pro Asn Arg Gln Gly Ser His Phe Met Pro Gly Ser Pro
          130          135          140
Leu Phe Arg Pro Gly Glu Lys Ala Ala Val Leu Thr Ser Thr Phe Ala
          145          150          155          160
Leu Ala Ala Phe Val Gly Phe Leu Gly Phe Leu Thr Trp Gln Phe Gly
          165          170          175
Trp Leu Phe Leu Leu Lys Phe Tyr Val Ala Pro Tyr Leu Val Phe Val
          180          185          190
Val Trp Leu Asp Leu Val Thr Phe Leu His His Thr Glu Asp Asn Ile
          195          200          205
Pro Trp Tyr Arg Gly Asp Asp Trp Tyr Phe Leu Lys Gly Ala Leu Ser
          210          215          220
Thr Ile Asp Arg Asp Tyr Gly Phe Ile Asn Pro Ile His His Asp Ile
          225          230          235          240
Gly Thr His Val Ala His His Ile Phe Ser Asn Met Pro His Tyr Lys
          245          250          255
Leu Arg Arg Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr
          260          265          270
Arg Tyr Ser Asp Glu Pro Ile Trp Gln Ala Phe Phe Lys Ser Tyr Trp
          275          280          285
Ala Cys His Phe Val Pro Asn Gln Gly Ser Gly Val Tyr Tyr Gln Ser
          290          295          300
Pro Ser Asn Gly Gly Tyr Gln Lys Lys Pro Xaa Leu Ile Leu Ile Glu
          305          310          315          320
Ser Asn Gln His Arg Glu Gly Arg Gln Tyr Xaa Met Val Leu Leu Pro
          325          330          335
Ser Asp Arg Leu Met Arg Ser Met Glu Val Lys Gln Ser His Ser
          340          345          350
Lys Arg Ser Ala Leu Asn Gln
          355

```

&lt;210&gt; 45

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Saprolegnia diclina

&lt;400&gt; 45

```

Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
 1          5          10          15
Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
 20          25          30
Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
 35          40          45
Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
 50          55          60
Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
 65          70          75          80
Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
 85          90          95
Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
100          105          110
Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
115          120          125
His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
130          135          140
Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145          150          155          160
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
165          170          175
Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
180          185          190
Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
195          200          205
Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
210          215          220
Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225          230          235          240
Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
245          250          255
Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
260          265          270
Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
275          280          285
Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
290          295          300
Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305          310          315          320
Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
325          330          335
Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
340          345          350
Ala Lys Ala Lys Ser Asp
355

```

&lt;210&gt; 46

&lt;211&gt; 409

&lt;212&gt; PRT

<213> *Caenorhabditis elegans*

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (389)...(389)

<223> Xaa = Unknown or Other at position 389

<400> 46

Val	Thr	Gly	Gly	Asp	Val	Leu	Val	Asp	Ala	Arg	Ala	Ser	Leu	Glu	Glu
1				5					10					15	
Lys	Glu	Ala	Pro	Arg	Asp	Val	Asn	Ala	Asn	Thr	Lys	Gln	Ala	Thr	Thr
			20					25					30		
Glu	Glu	Pro	Arg	Ile	Gln	Leu	Pro	Thr	Val	Asp	Ala	Phe	Arg	Arg	Ala
			35					40				45			
Ile	Pro	Ala	His	Cys	Phe	Glu	Arg	Asp	Leu	Val	Lys	Ser	Ile	Arg	Tyr
	50					55					60				
Leu	Val	Gln	Asp	Phe	Ala	Ala	Leu	Thr	Ile	Leu	Tyr	Phe	Ala	Leu	Pro
65					70					75					80
Ala	Phe	Glu	Tyr	Phe	Gly	Leu	Phe	Gly	Tyr	Leu	Val	Trp	Asn	Ile	Phe
				85					90					95	
Met	Gly	Val	Phe	Gly	Phe	Ala	Leu	Phe	Val	Val	Gly	His	Asp	Cys	Leu
			100					105					110		
His	Gly	Ser	Phe	Ser	Asp	Asn	Gln	Asn	Leu	Asn	Asp	Phe	Ile	Gly	His
		115					120					125			
Ile	Ala	Phe	Ser	Pro	Leu	Phe	Ser	Pro	Tyr	Phe	Pro	Trp	Gln	Lys	Ser
	130					135					140				
His	Lys	Leu	His	His	Ala	Phe	Thr	Asn	His	Ile	Asp	Lys	Asp	His	Gly
145					150					155					160
His	Val	Trp	Ile	Gln	Asp	Lys	Asp	Trp	Glu	Ala	Met	Pro	Ser	Trp	Lys
				165					170					175	
Arg	Trp	Phe	Asn	Pro	Ile	Pro	Phe	Ser	Gly	Trp	Leu	Lys	Trp	Phe	Pro
			180					185					190		
Val	Tyr	Thr	Leu	Phe	Gly	Phe	Cys	Asp	Gly	Ser	His	Phe	Trp	Pro	Tyr
		195					200					205			
Ser	Ser	Leu	Phe	Val	Arg	Asn	Ser	Asp	Arg	Val	Gln	Cys	Val	Ile	Ser
	210					215					220				
Gly	Ile	Cys	Cys	Cys	Val	Cys	Ala	Tyr	Ile	Ala	Leu	Thr	Ile	Ala	Gly
225					230					235					240
Ser	Tyr	Ser	Asn	Trp	Phe	Trp	Tyr	Tyr	Trp	Val	Pro	Leu	Ser	Phe	Phe
			245						250					255	
Gly	Leu	Met	Leu	Val	Ile	Val	Thr	Tyr	Leu	Gln	His	Val	Asp	Asp	Val
			260					265					270		
Ala	Glu	Val	Tyr	Glu	Ala	Asp	Glu	Trp	Ser	Phe	Val	Arg	Gly	Gln	Thr
		275					280					285			
Gln	Thr	Ile	Asp	Arg	Tyr	Tyr	Gly	Leu	Gly	Leu	Asp	Thr	Thr	Met	His
	290					295					300				
His	Ile	Thr	Asp	Gly	His	Val	Ala	His	His	Phe	Phe	Asn	Lys	Ile	Pro
305					310					315					320
His	Tyr	His	Leu	Ile	Glu	Ala	Thr	Glu	Gly	Val	Lys	Lys	Val	Leu	Glu
			325						330					335	
Pro	Leu	Ser	Asp	Thr	Gln	Tyr	Gly	Tyr	Lys	Ser	Gln	Val	Asn	Tyr	Asp
			340					345					350		
Phe	Phe	Ala	Arg	Phe	Leu	Trp	Phe	Asn	Tyr	Lys	Leu	Asp	Tyr	Leu	Val
		355					360					365			
His	Lys	Thr	Ala	Gly	Ile	Met	Gln	Phe	Arg	Thr	Thr	Leu	Glu	Glu	Lys
	370					375					380				
Ala	Lys	Ala	Lys	Xaa	Lys	Asn	Ile	Pro	Cys	Arg	Ser	Arg	Val	Gln	Gln
385					390					395					400
Gln	Leu	Leu	Arg	Phe	His	Arg	Phe	Cys							
				405											

<210> 47

&lt;211&gt; 333

&lt;212&gt; PRT

<213> *Saprolegnia diclina*

&lt;400&gt; 47

```

Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
 1      5      10      15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
 20      25      30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
 35      40      45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
 50      55      60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
 65      70      75      80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
 85      90      95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
 100     105     110
Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
 115     120     125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
 130     135     140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
 145     150     155     160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
 165     170     175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
 180     185     190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
 195     200     205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
 210     215     220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
 225     230     235     240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
 245     250     255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
 260     265     270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
 275     280     285
Thr Pro Leu Leu Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro
 290     295     300
Leu Ala Leu Trp Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp
 305     310     315     320
Gly Asn Val Val Phe Tyr Lys Arg Lys Leu Glu Glu Lys
 325     330

```

&lt;210&gt; 48

&lt;211&gt; 412

&lt;212&gt; PRT

<213> *Gossypium hirsutum*

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (9)...(9)

&lt;223&gt; Xaa = Unknown or Other at position 9

&lt;221&gt; VARIANT

&lt;222&gt; (403)...(403)

&lt;223&gt; Xaa = Unknown or Other at position 403

&lt;400&gt; 48

```

Leu Arg Val Ser Ser Thr Trp Arg Xaa Thr Ala Phe Phe Lys Ala Ser
 1          5          10          15
Lys Met Gly Ala Gly Gly Arg Met Pro Ile Asp Gly Ile Lys Glu Glu
          20          25          30
Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys Pro Pro Phe Thr
          35          40          45
Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys Phe Arg Arg Ser
 50          55          60
Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu Cys Leu Ala Ser
 65          70          75          80
Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe Leu Pro Gln Pro
          85          90          95
Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu Gln Gly Cys Ile
          100          105          110
Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly His His Ala Phe
          115          120          125
Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
 130          135          140
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His
 145          150          155          160
His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val Phe Val Pro Lys
          165          170          175
Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu Asn Asn Pro Pro
          180          185          190
Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu Gly Trp Pro Met
          195          200          205
Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Leu Ala Ser
 210          215          220
His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
 225          230          235          240
Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile Tyr Val Leu Tyr
          245          250          255
Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu Cys Thr Tyr Gly
          260          265          270
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
          275          280          285
Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 290          295          300
Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp Phe Gly Val Leu
 305          310          315          320
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
          325          330          335
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
          340          345          350
Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly Thr Pro Ile Tyr
          355          360          365
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
 370          375          380
Val Gly Gly Gly Gly Gly Ser Lys Gly Val Phe Trp Tyr Arg Asn
 385          390          395          400
Lys Phe Xaa Arg Pro Thr Asn Cys Leu Ile Ala Gly

```

405

410

&lt;210&gt; 49

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein Motif 1 from Example 3

&lt;400&gt; 49

Thr	Arg	Ala	Ala	Ile	Pro	Lys	His	Cys	Trp	Val	Lys
1				5					10		

&lt;210&gt; 50

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein Motif 2 from Example 3

&lt;400&gt; 50

Ala	Leu	Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser
1				5					10					15

&lt;210&gt; 51

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein Motif 3 from Example 3

&lt;400&gt; 51

Pro	Tyr	His	Gly	Trp	Arg	Ile	Ser	His	Arg	Thr	His	His	Gln	Asn
1				5					10					15

&lt;210&gt; 52

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Protein Motif 4 from Example 3

&lt;221&gt; VARIANT

&lt;222&gt; (5)...(5)

&lt;223&gt; Xaa = D or H at position 5

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(7)

&lt;223&gt; Xaa = D or Y at position 7

&lt;400&gt; 52

Gly	Ser	His	Phe	Xaa	Pro	Xaa	Ser	Asp	Leu	Phe	Val
1				5					10		



<210> 53  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein Motif 5 from Example 3

<221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = Y or F at position 3

<221> VARIANT  
 <222> (4)...(4)  
 <223> Xaa = L or V at position 4

<221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = L or I at position 11

<400> 53  
 Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg  
       1                  5                  10

<210> 54  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein Motif 6 from Example 3

<400> 54  
 His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln  
       1                  5                  10                  15

<210> 55  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein Motif 7 from Example 3

<221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = L or F at position 2

<221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Q or K at position 5

<221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = V or I at position 12

<400> 55

His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr  
 1 5 10 15

<210> 56

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 8 from Example 3

<221> VARIANT

<222> (3)...(3)

<223> Xaa = A or I at position 3

<221> VARIANT

<222> (6)...(6)

<223> Xaa = L or F at position 6

<400> 56

His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu  
 1 5 10 15

<210> 57

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 1 from Example 7

<221> VARIANT

<222> (2)...(2)

<223> Xaa = N or E at position 2

<221> VARIANT

<222> (10)...(10)

<223> Xaa = D or E at position 10

<221> VARIANT

<222> (11)...(11)

<223> Xaa = A or C at position 11

<400> 57

Pro Xaa Phe Thr Ile Lys Glu Ile Arg Xaa Xaa Ile Pro Ala His Cys  
 1 5 10 15  
 Phe

<210> 58

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 2 from Example 7

<221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = H or F at position 3

<221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = V or Y at position 11

<221> VARIANT  
 <222> (13)...(13)  
 <223> Xaa = I or L at position 13

<221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = A or L at position 16

<400> 58  
 Met Pro Xaa Tyr His Ala Glu Glu Ala Thr Xaa His Xaa Lys Lys Xaa  
     1                    5                    10                    15

<210> 59  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Protein Motif 3 from Example 7

<221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = L or V at position 2

<221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = A or I at position 5

<221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = C or M or A at position 6

<221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = V or I at position 9

<221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = L or G or C at position 11

<400> 59  
 Pro Xaa Tyr Trp Xaa Xaa Gln Gly Xaa Val Xaa Thr Gly Val Trp  
     1                    5                    10                    15

<210> 60  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Protein Motif 4 from Example 7

<221> VARIANT

<222> (6)...(6)

<223> Xaa = L or F at position 6

<221> VARIANT

<222> (9)...(9)

<223> Xaa = T or Q at position 9 .

<400> 60

His	Val	Ala	His	His	Xaa	Phe	Ser	Xaa	Met	Pro	His	Tyr	His	Ala
1				5					10					15